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mORK1 MESPIQIFRGDPGPTCSPSACLLPNSSSW:::FPNWAESDSNGSVGSEDQQLESAHISPAIPVIITAVY 66
**          *** |**          ** *          ** *          *| | ***|*
mORD1 ME:::LVPSARAELOSSPLVNLSDAFP SAFP SAGANASGSPGARSASSL:::ALAIATIALY 56
          TM2
mORK1 SVVFFVGLVGNLSVMFVIRYTKMKTATNIYIFNLALADALVTTTTFQSAVYLMNSWPFQDVLCKIVISID 138
* * ***|** ***** *|****|*****|***** *|*|***** *** |****|*** *|***
mORD1 SAVCAVGLLGNVLMFVIRYTKLKTATNIYIFNLALADALATSTLFQSAKYLMETWPFQELLCKAVLSID 128
          TM3
mORK1 YYNMFTSIFTLTMSVDRYIAVCHPVKALDFRTPKAKIINICIWLLASSVGISAIVLGGTKVREDVDVIEC 210
*****|*****|*** **| |*| * *| * *
mORD1 YYNMFTSIFTLTMSVDRYIAVCHPVKALDFRTPAKAKLINICIWVLASGVGVFIMVMAVTQPRDGAVV::C 198
          TM 5
mORK1 SLQFPDDEYSWWDLFMKICVFVFAFVIPVLIIIVCYTLMILRLKSVRLLSGSREKDRNLRRITKLVLVVAV 282
**** | |** *****|****|*|*** *** **|***|*****|*****|*****|*****
mORD1 MLQFPSPSW:YWDTVTKICVFLFAFVVPILIIITVCYGLMLLRLRSVRLLSGSKEKDRSLRRITRMVLVVGA 269
          TM 6
mORK1 FIICWTPIHIFILVEALGSTSHSTAALSSYY:FCIALGYTNSSLNPVLYAFDENFKRCFRDFCFPIKMRME 353
*|** *****|* *          |*****|*****|*****|*****|*****|*****
mORD1 FVVCWAPIHIFVIVWTLVDINRRDPLVVAALHLCIALGYANSSLPVLYAFDENFKRCFRQLCRTPCGRQE 341
          TM 7
mORK1 RQSTNRVRNTVQDP:::ASMRDVGGMNKPV - 380 (SEQ ID NO:2)
* * *|          | * *
mORD1 PGSLRRPRQATTRERVACTP SDGPGGGAAA - 372 (SEQ ID NO:4)

```

FIG. 1

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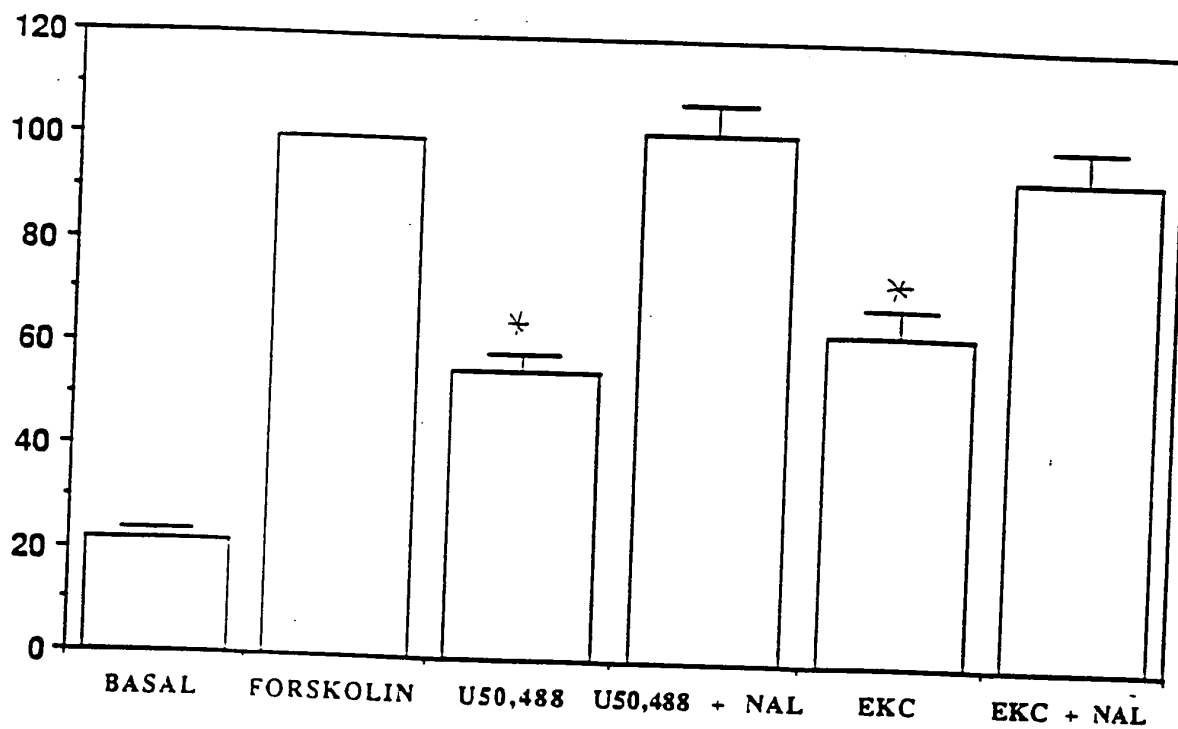


FIG. 2a

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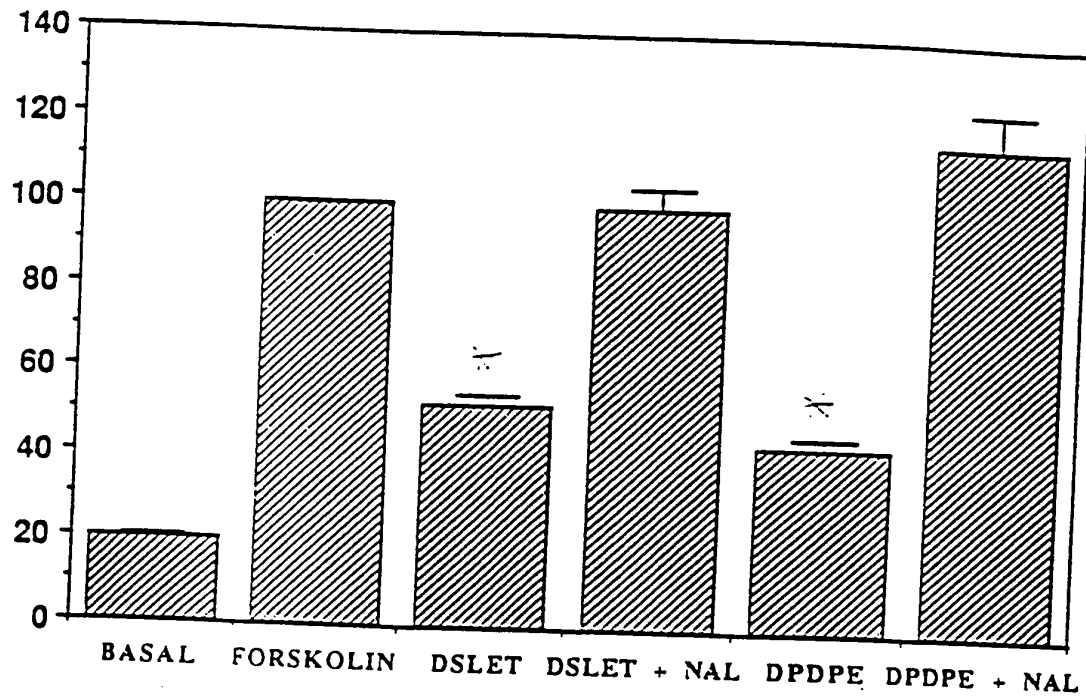


FIG. 2b

1 AAGAAGCAAAATCAGTAATCCAAAGGCTATCACAAACACATTACCTTATGGGGTTTGAC
 61 TTGAAAATGGAGGGAAATGCTATTGTTTCTTTCTTTTAGATACACAAAGATGAAGACAG
 TyrThrLysMetLysThrAla
 121 ThrAsnIleTyrIlePheAsnLeuAlaLeuAlaAspAlaLeuValThrThrThrMetPro
 CAACCAACATTTACATATTTAACCTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGC
 181 PheGlnSerThrValTyrLeuMetAsnSerTrpProPheGlyAspValLeuCysLysIle
 CCTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGA
 241 ValIleSerIleAspTyrTyrAsnMetPheThrSerIlePheThrLeuThrMetMetSer
 TAGTAATTTCCATTGATTACTACAACATGTTCCACCAGCATCTTCACCTTGACCATGATGA
 301 ValAspArgTyrIleAlaValCysHisProValLysAlaLeuAspPheArgThrProLeu
 GCGTGGACCGCTACATTGCCGTGTGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCT
 361 LysAlaLysIleIleAsnIleCysIleTrpLeuLeuSerSerSerValGlyIleSerAla
 TGAAGGCAAAGATCATCAATATCTGCATCTGGCTGCTGTCTGTCATCTGTGGCATCTCTG
 421 IleValLeuGlyGlyThrLysValArgGluA
 CAATAGTCCTTGGAGGCACCAAAGTCAGGGAAGGT::::::::::::TTTCTGTGTTGT
 481 spValAspValIleGluCysCysLeuGlnPheProAsp
 GGTTTTTATTGCCCTCCTCCAGACGTCGATGTCATTGAGTGCTGCTGCAGTTCCAGAT
 541 AspAspTyrSerTrpTrpAspLeuPheMetLysIleCysValPheIlePheAlaPheVal
 GATGACTACTCCTGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTGCCTTCGTG
 601 IleProValLeuIleIleIleValCysTyrThrLeuMetIleLeuArgLeuLysNNNVal
 ATCCCTGTCCTCATCATCATCGTCTGCTACACCCTGATGATCCTGCGTCTCAAGANNGTC
 661 ArgLeuLeuSerGlySerArgGluLysAspNNNAsnLeuArgArgIleThrArgLeuVal
 CGGCTCCTTTCTGGCTCCCGAGAGAAAGATNNCAACCTGCGTAGGATCACCAGACTGGTC
 721 LeuValValValAlaValPheValValCysTrpThrProIleHisIlePheIleLeuVal
 CTGGTGGTGGTGGCAGTCTTCGTCGTCTGCTGGACTCCCATTCACATATTCATCCTGGTG
 781 GluAlaLeuGlySerThrSerHisSerThrAlaAlaLeuSerSerTyrTyrPheCysIle
 GAGGCTCTGGGGAGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATC
 841 AlaLeuGlyTyrThrAsnSerSerLeuAsnProIleLeuTyrAlaPheLeuAspGluAsn
 GCCTTAGGCTATACCAACAGTAGCCTGAATCCCATCTCTACGCCTTCTTGATGAAAAC
 901 PheLysArgCysPheArgAspPheCysPheProLeuLysMetNNNMetGluArgNNNSer
 TTCAAGCGGTGTTTCCGGGACTTCTGCTTTCCACTGAAGATGAGNATGGAGCGCNAGAGC
 961 ThrSerArgValArgAsnThrValGlnAspProAlaTyrLeuArgGluIleAspGlyMet
 ACTAGCAGAGTCCGAAATACAGTTCAGGATCCTGCTTACCTGAGGGAGATCGATGGGATG
 1021 MetAsnLysProValop (SEQ ID NO:12)
 ATGAATAAACCACTATGACTAGTCGTGGA (SEQ ID NO:11)

FIG. 3

	Met	Glu	Ser	Pro	Ile	Gln	Ile	Phe	Arg	Gly	Asp	Pro	Gly	Pro	Thr	Cys
	1				5					10					15	
	Ser	Pro	Ser	Ala	Cys	Leu	Leu	Pro	Asn	Ser	Ser	Ser	Trp	Phe	Pro	Asn
				20					25					30		
	Trp	Ala	Glu	Ser	Asp	Ser	Asn	Gly	Ser	Val	Gly	Ser	Glu	Asp	Gln	Gln
			35					40					45			
	Leu	Glu	Ser	Ala	His	Ile	Ser	Pro	Ala	Ile	Pro	Val	Ile	Ile	Thr	Ala
		50					55					60				
	Val	Tyr	Ser	Val	Val	Phe	Val	Val	Gly	Leu	Val	Gly	Asn	Ser	Leu	Val
	65					70					75					80
HUMAN																
MOUSE	Met	Phe	Val	Ile	Ile	Arg	Tyr	Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile
					85					90					95	
HUMAN	Tyr	Ile	Phe	Asn	Leu	Ala	Leu	Ala	Asp	Ala	Leu	Val	Thr	Thr	Thr	Met
MOUSE	Tyr	Ile	Phe	Asn	Leu	Ala	Leu	Ala	Asp	Ala	Leu	Val	Thr	Thr	Thr	Met
				100					105					110		
HUMAN	Pro	Phe	Gln	Ser	Thr	Val	Tyr	Leu	Met	Asn	Ser	Trp	Pro	Phe	Gly	Asp
MOUSE	Pro	Phe	Gln	Ser	Ala	Val	Tyr	Leu	Met	Asn	Ser	Trp	Pro	Phe	Gly	Asp
			115					120					125			
HUMAN	Val	Leu	Cys	Lys	Ile	Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr
MOUSE	Val	Leu	Cys	Lys	Ile	Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr
		130					135					140				
HUMAN	Ser	Ile	Phe	Thr	Leu	Thr	Met	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val
MOUSE	Ser	Ile	Phe	Thr	Leu	Thr	Met	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val
	145					150					155					160
HUMAN	Cys	His	Pro	Val	Lys	Ala	Leu	Asp	Phe	Arg	Thr	Pro	Leu	Lys	Ala	Lys
MOUSE	Cys	His	Pro	Val	Lys	Ala	Leu	Asp	Phe	Arg	Thr	Pro	Leu	Lys	Ala	Lys
					165				170						175	
HUMAN	Ile	Ile	Asn	Ile	Cys	Ile	Trp	Leu	Leu	Ser	Ser	Ser	Val	Gly	Ile	Ser
MOUSE	Ile	Ile	Asn	Ile	Cys	Ile	Trp	Leu	Leu	Ala	Ser	Ser	Val	Gly	Ile	Ser
				180				185						190		
HUMAN	Ala	Ile	Val	Leu	Gly	Gly	Thr	Lys	Val	Arg	Glu	Asp	Val	Asp	Val	Ile
MOUSE	Ala	Ile	Val	Leu	Gly	Gly	Thr	Lys	Val	Arg	Glu	Asp	Val	Asp	Val	Ile
			195					200					205			
HUMAN	Glu	Cys	Cys	Leu	Gln	Phe	Pro	Asp	Asp	Asp	Tyr	Ser	Trp	Trp	Asp	Leu
MOUSE	Glu	Cys	Ser	Leu	Gln	Phe	Pro	Asp	Asp	Glu	Tyr	Ser	Trp	Trp	Asp	Leu
		210					215					220				
HUMAN	Phe	Met	Lys	Ile	Cys	Val	Phe	Ile	Phe	Ala	Phe	Val	Ile	Pro	Val	Leu
MOUSE	Phe	Met	Lys	Ile	Cys	Val	Phe	Val	Phe	Ala	Phe	Val	Ile	Pro	Val	Leu
	225					230					235					240
HUMAN	Ile	Ile	Ile	Val	Cys	Tyr	Thr	Leu	Met	Ile	Leu	Arg	Leu	Lys	NNN	Val
MOUSE	Ile	Ile	Ile	Val	Cys	Tyr	Thr	Leu	Met	Ile	Leu	Arg	Leu	Lys	Ser	Val
					245					250					255	

FIG. 4a

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HUMAN	Arg	Leu	Leu	Ser	Gly	Ser	Arg	Glu	Lys	Asp	NNN	Asn	Leu	Arg	Arg	Ile
MOUSE	Arg	Leu	Leu	Ser	Gly	Ser	Arg	Glu	Lys	Asp	Arg	Asn	Leu	Arg	Arg	Ile
				260					265					270		
HUMAN	Thr	Arg	Leu	Val	Leu	Val	Val	Val	Ala	Val	Phe	Val	Val	Cys	Trp	Thr
MOUSE	Thr	Lys	Leu	Val	Leu	Val	Val	Val	Ala	Val	Phe	Ile	Ile	Cys	Trp	Thr
			275					280					285			
HUMAN	Pro	Ile	His	Ile	Phe	Ile	Leu	Val	Glu	Ala	Leu	Gly	Ser	Thr	Ser	His
MOUSE	Pro	Ile	His	Ile	Phe	Ile	Leu	Val	Glu	Ala	Leu	Gly	Ser	Thr	Ser	His
		290					295					300				
HUMAN	Ser	Thr	Ala	Ala	Leu	Ser	Ser	Tyr	Tyr	Phe	Cys	Ile	Ala	Leu	Gly	Tyr
MOUSE	Ser	Thr	Ala	Ala	Leu	Ser	Ser	Tyr	Tyr	Phe	Cys	Ile	Ala	Leu	Gly	Tyr
	305					310					315				320	
HUMAN	Thr	Asn	Ser	Ser	Leu	Asn	Pro	Ile	Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn
MOUSE	Thr	Asn	Ser	Ser	Leu	Asn	Pro	Val	Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn
					325					330				335		
HUMAN	Phe	Lys	Arg	Cys	Phe	Arg	Asp	Phe	Cys	Phe	Pro	Leu	Lys	Met	NNN	Met
MOUSE	Phe	Lys	Arg	Cys	Phe	Arg	Asp	Phe	Cys	Phe	Pro	Ile	Lys	Met	Arg	Met
				340					345					350		
HUMAN	Glu	Arg	NNN	Ser	Thr	Ser	Arg	Val	Arg	Asn	Thr	Val	Gln	Asp	Pro	Ala
MOUSE	Glu	Arg	Gln	Ser	Thr	Asn	Arg	Val	Arg	Asn	Thr	Val	Gln	Asp	Pro	Ala
			355					360					365			
HUMAN	Tyr	Leu	Arg	Glu	Ile	Asp	Gly	Met	Met	Asn	Lys	Pro	Val			(SEQ ID NO:12)
MOUSE		Ser	Met	Arg	Asp	Val	Gly	Gly	Met	Asn	Lys	Pro	Val			(SEQ ID NO:2)
			370					375					380			

FIG. 4b

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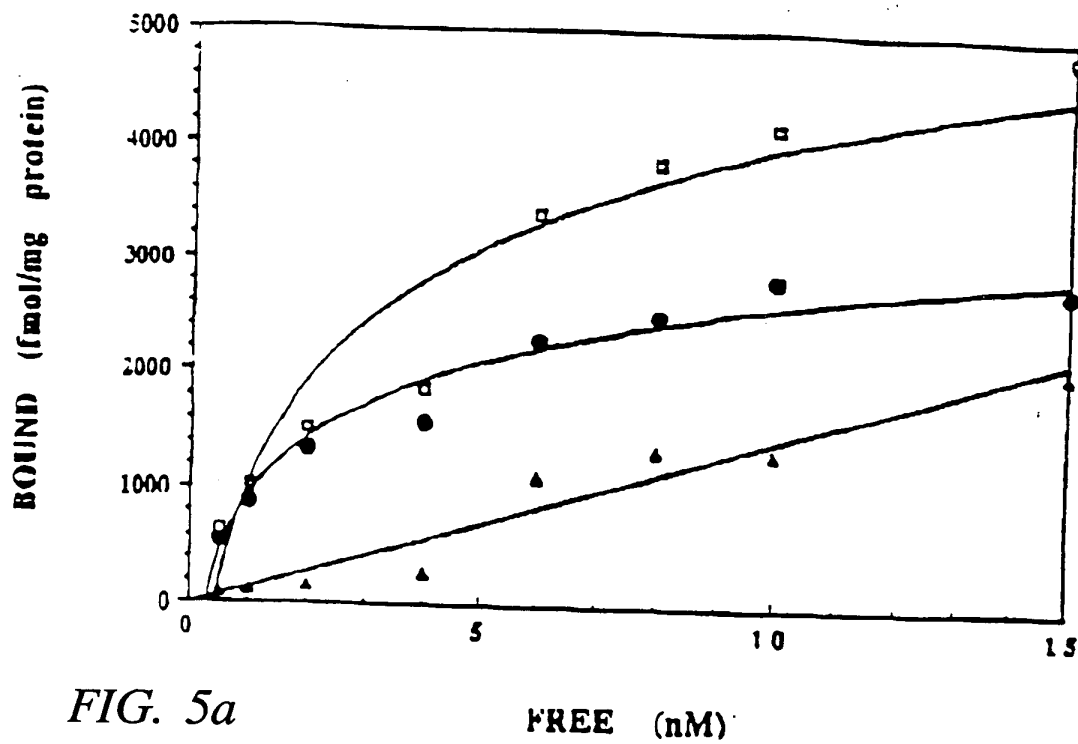


FIG. 5a

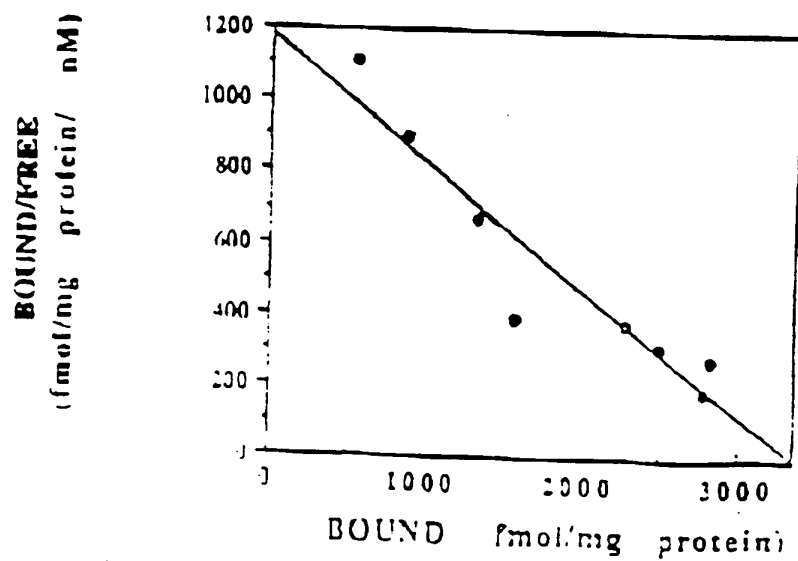


FIG. 5b

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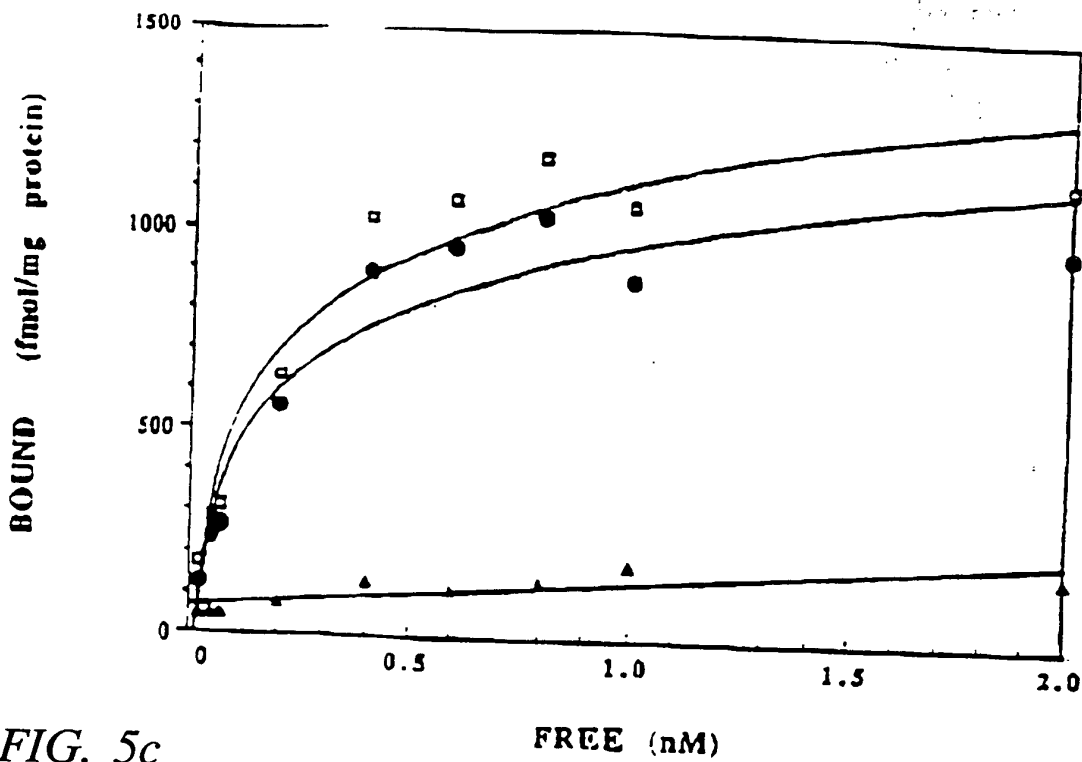


FIG. 5c

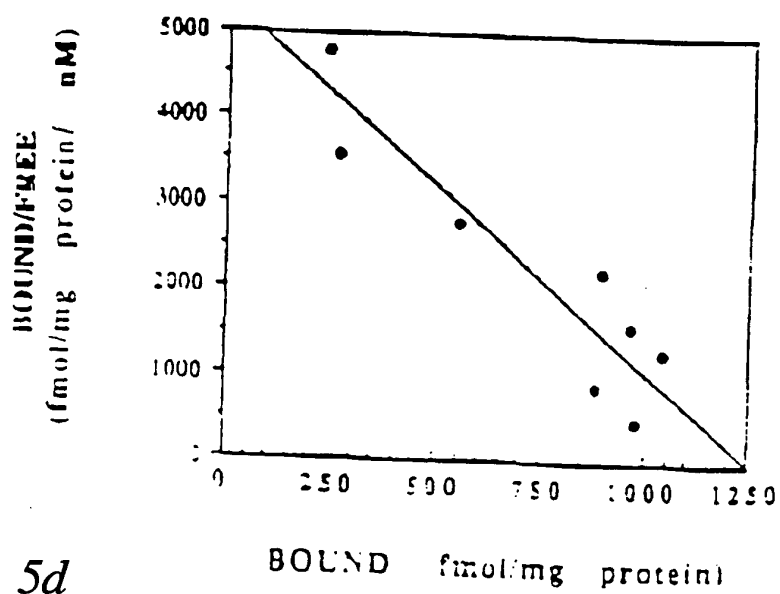


FIG. 5d

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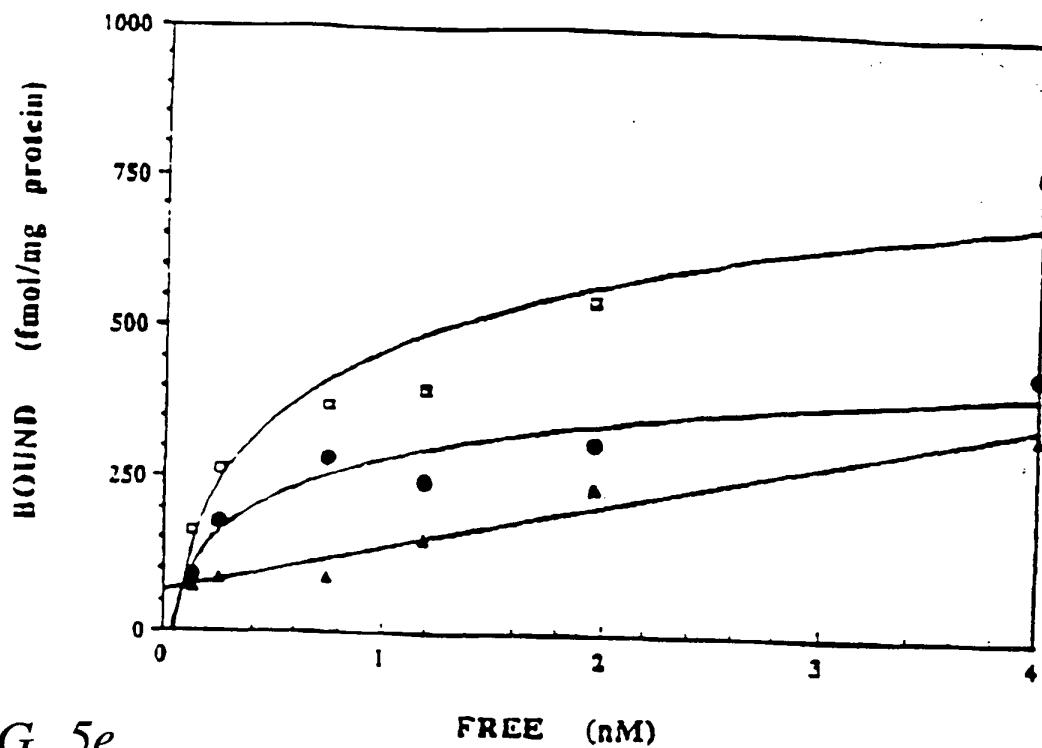


FIG. 5e

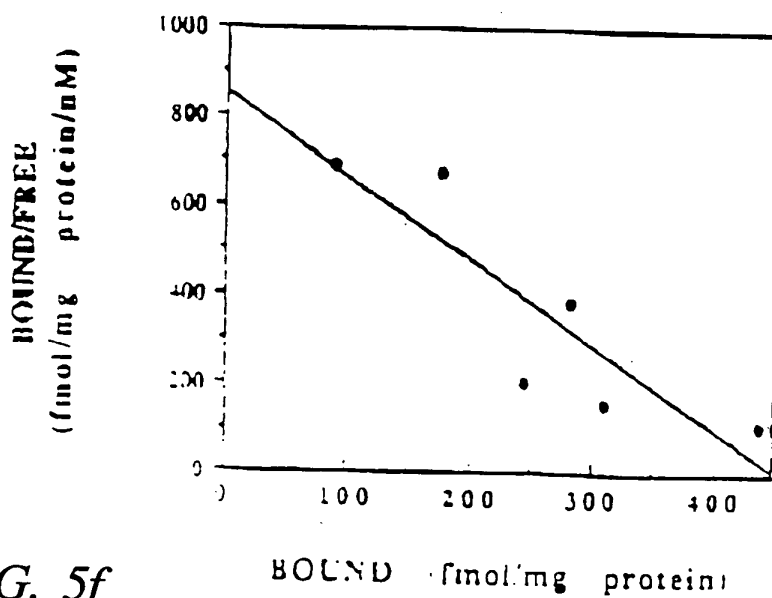


FIG. 5f

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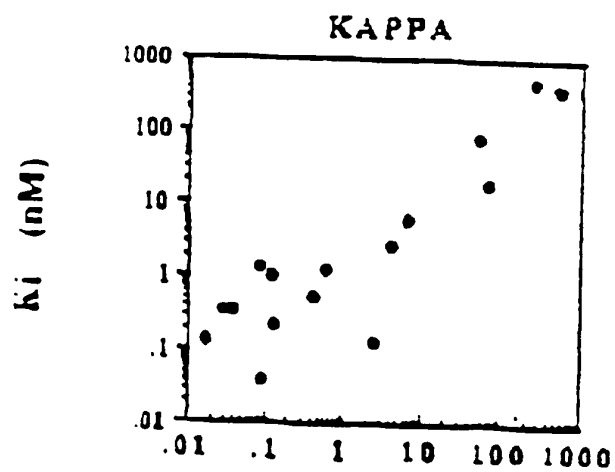


FIG. 6a

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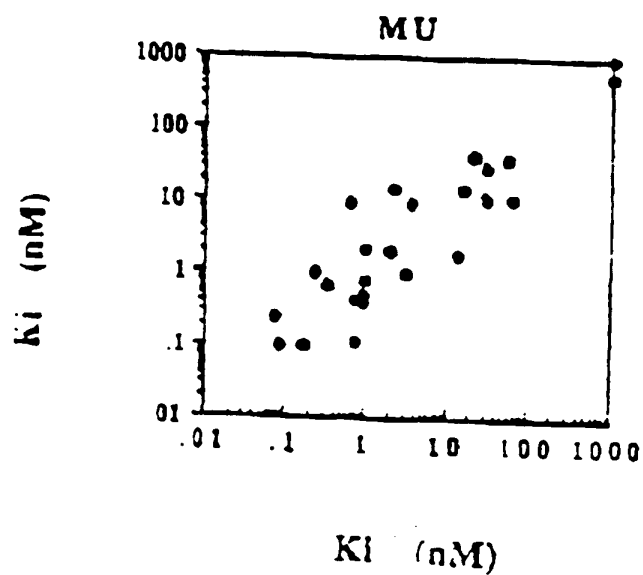


FIG. 6b

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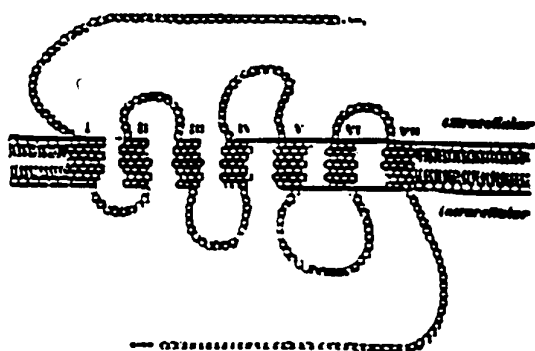


FIG. 7a

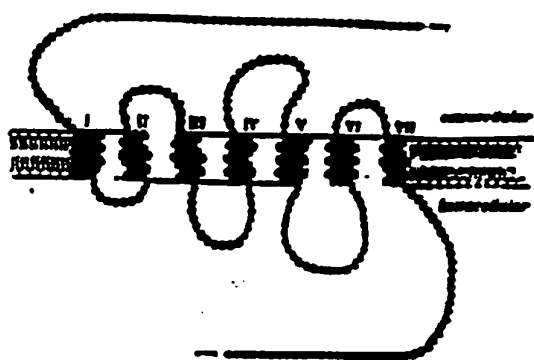


FIG. 7b

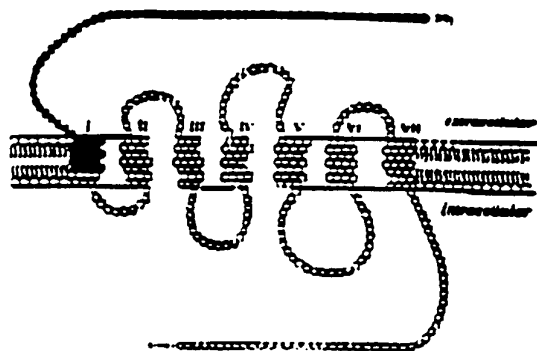


FIG. 7c

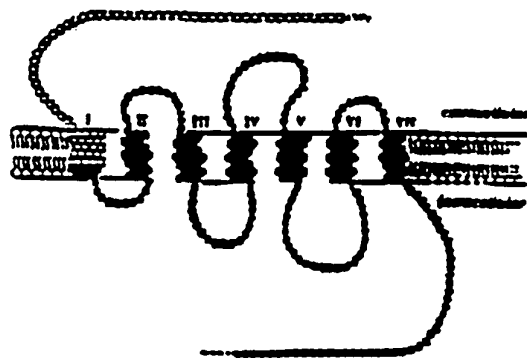


FIG. 7d

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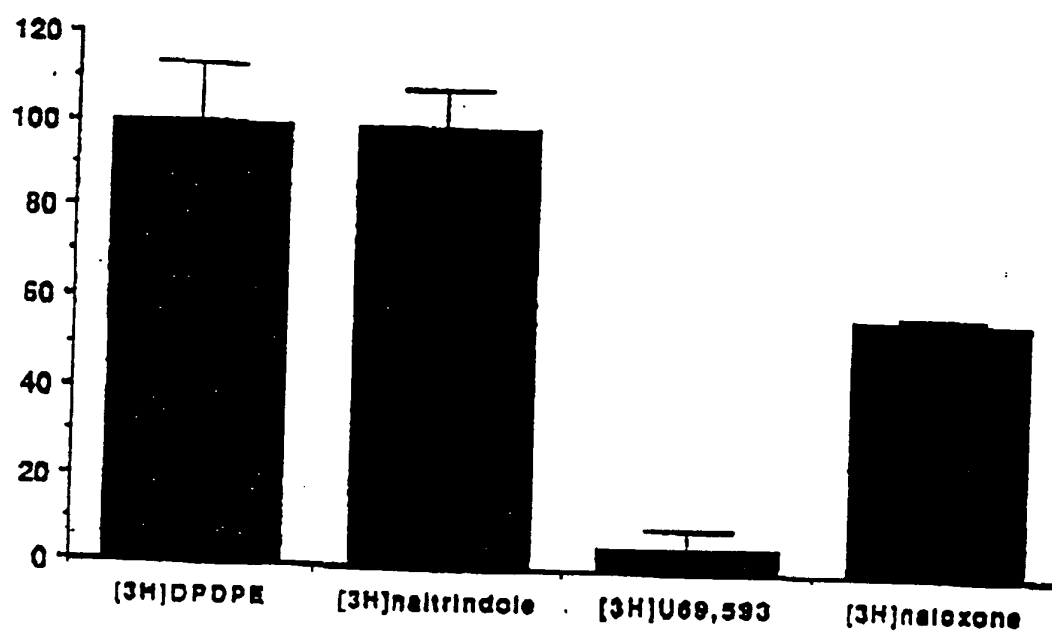


FIG. 8

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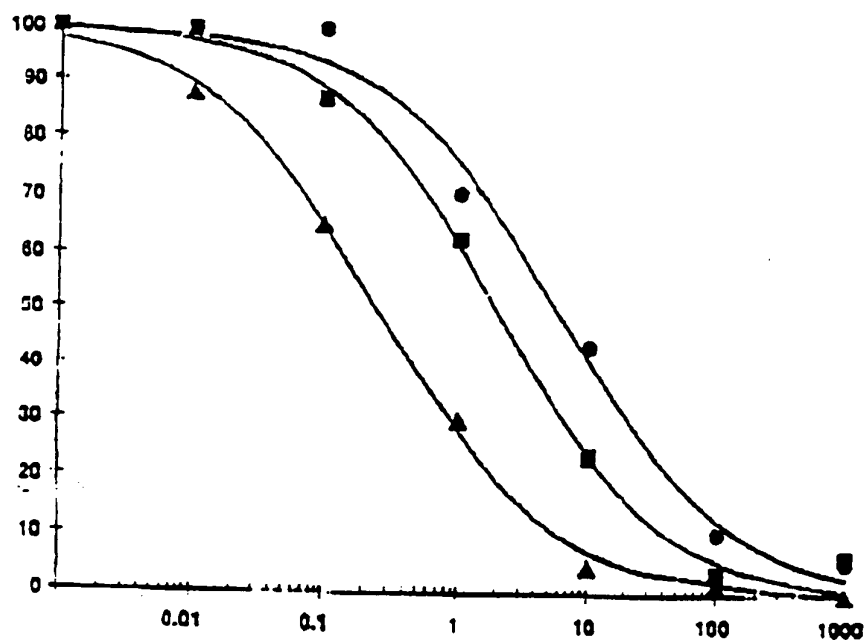


FIG. 9a

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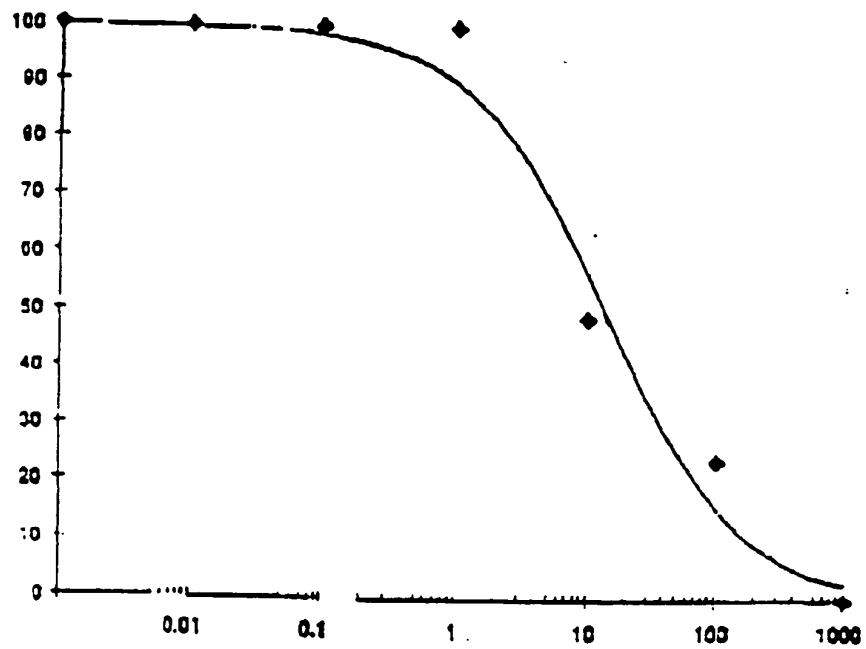


FIG. 9b

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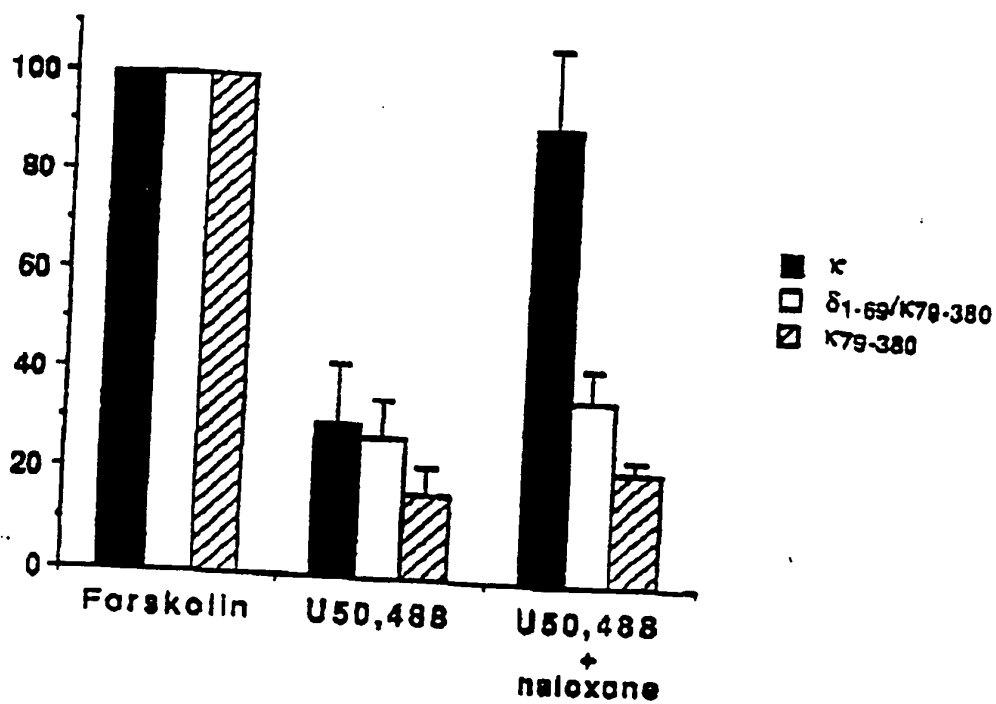


FIG. 10a

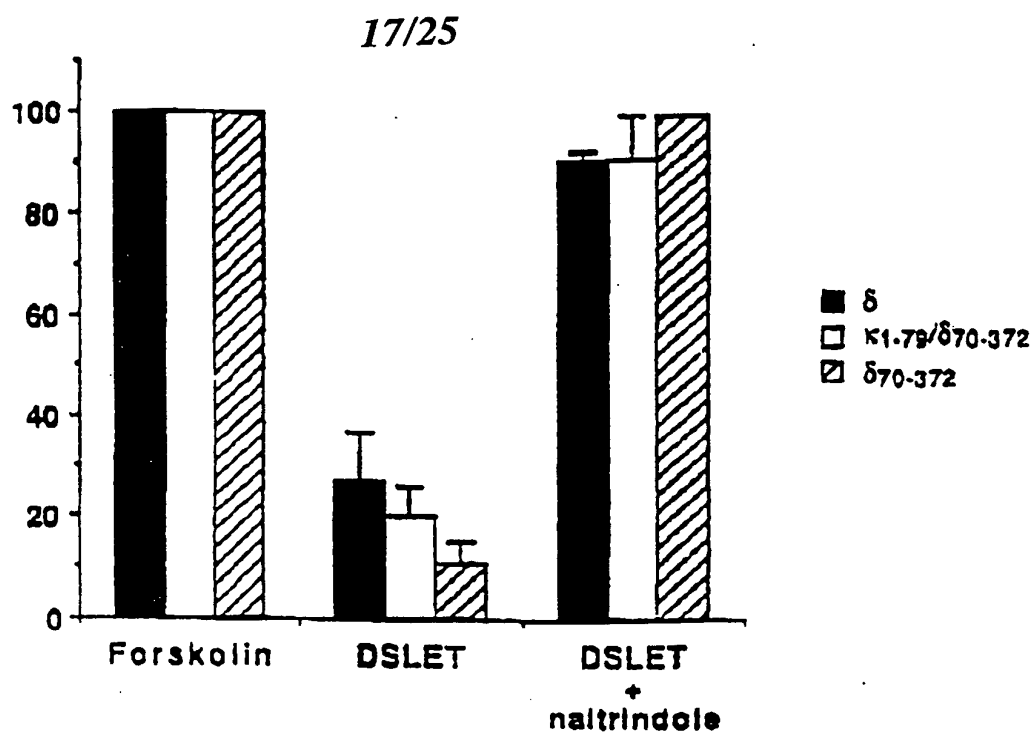


FIG. 10b

FIG. 11a

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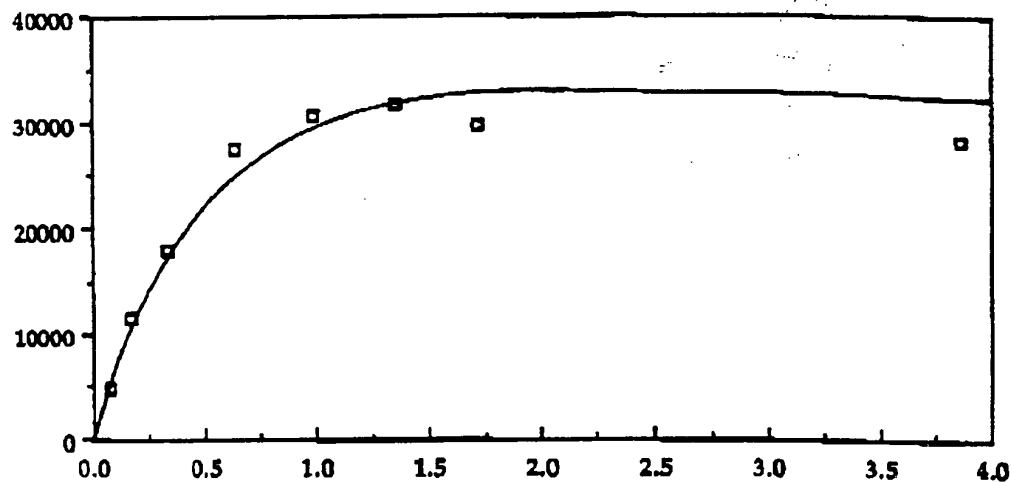


FIG. 11b

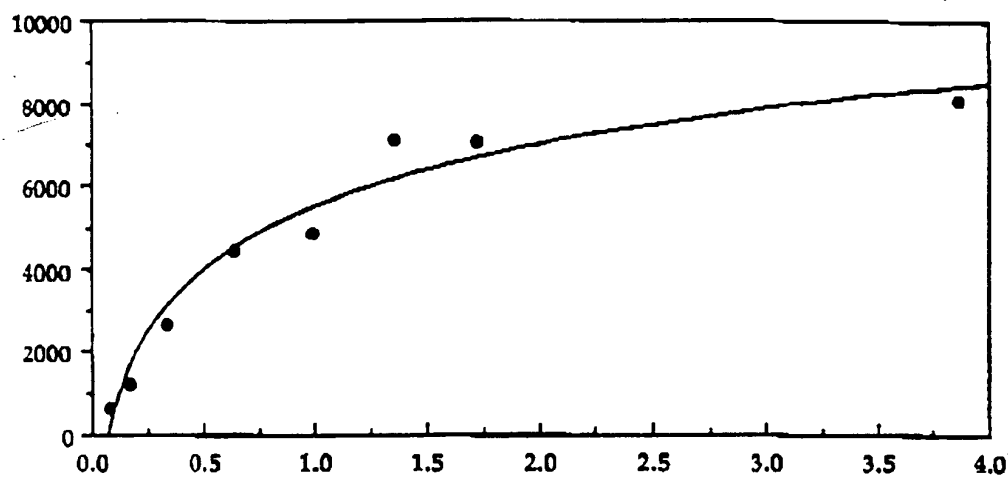
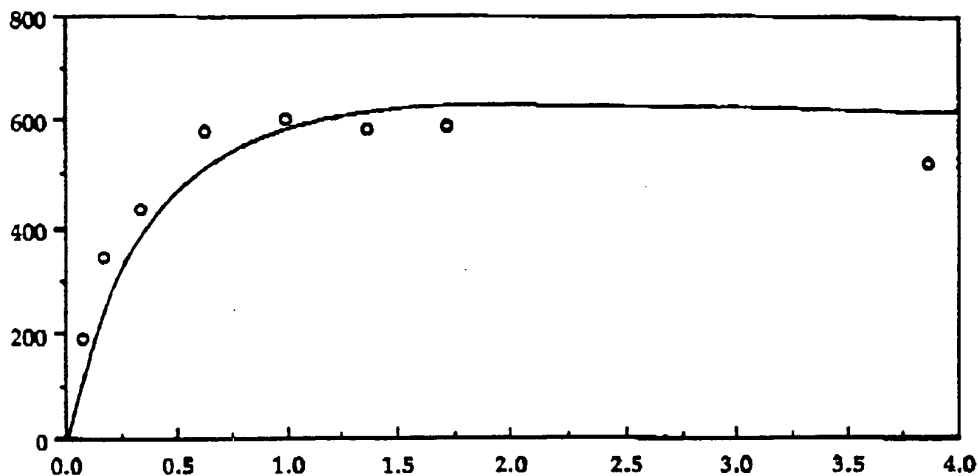


FIG. 11c



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FIG. 12a

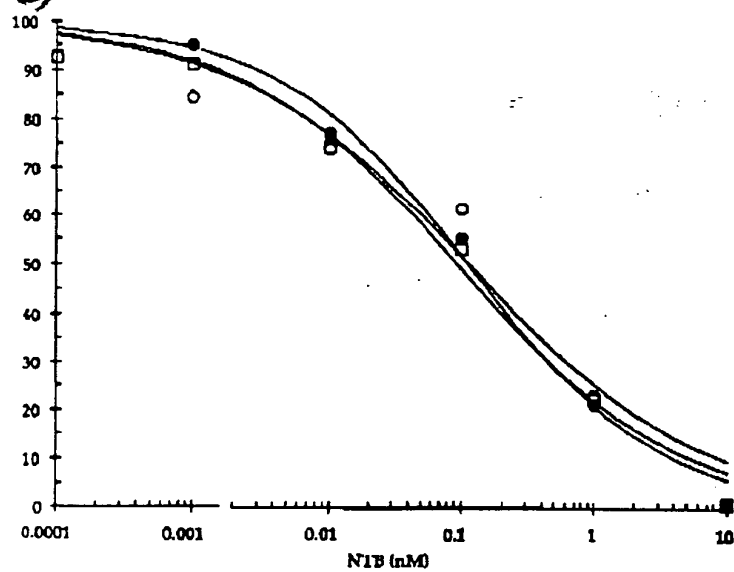


FIG. 12b

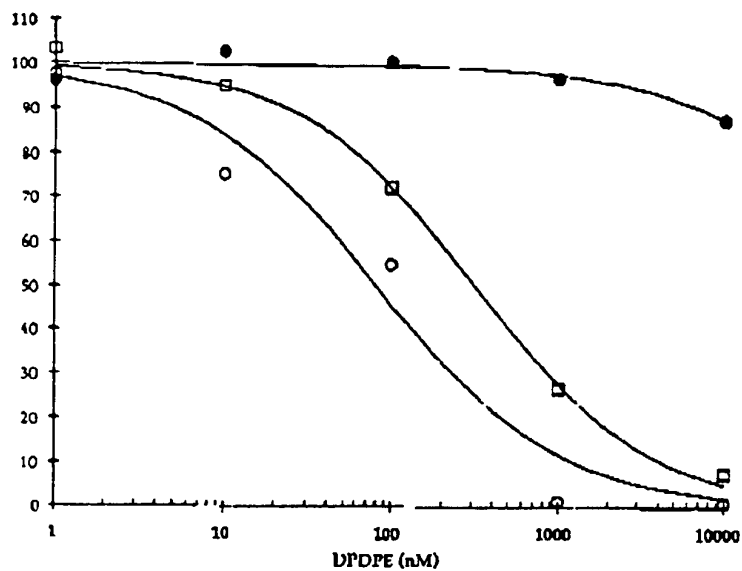
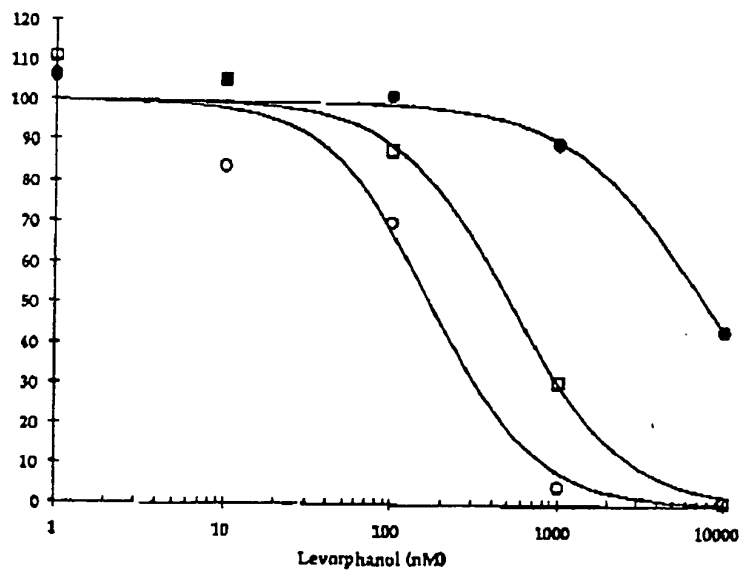


FIG. 12c



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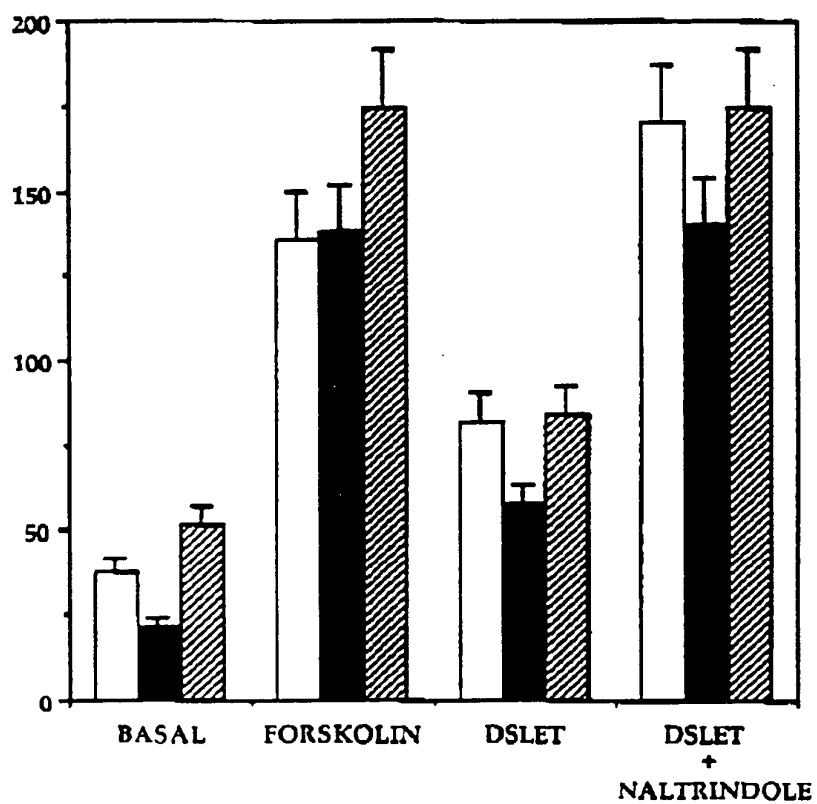
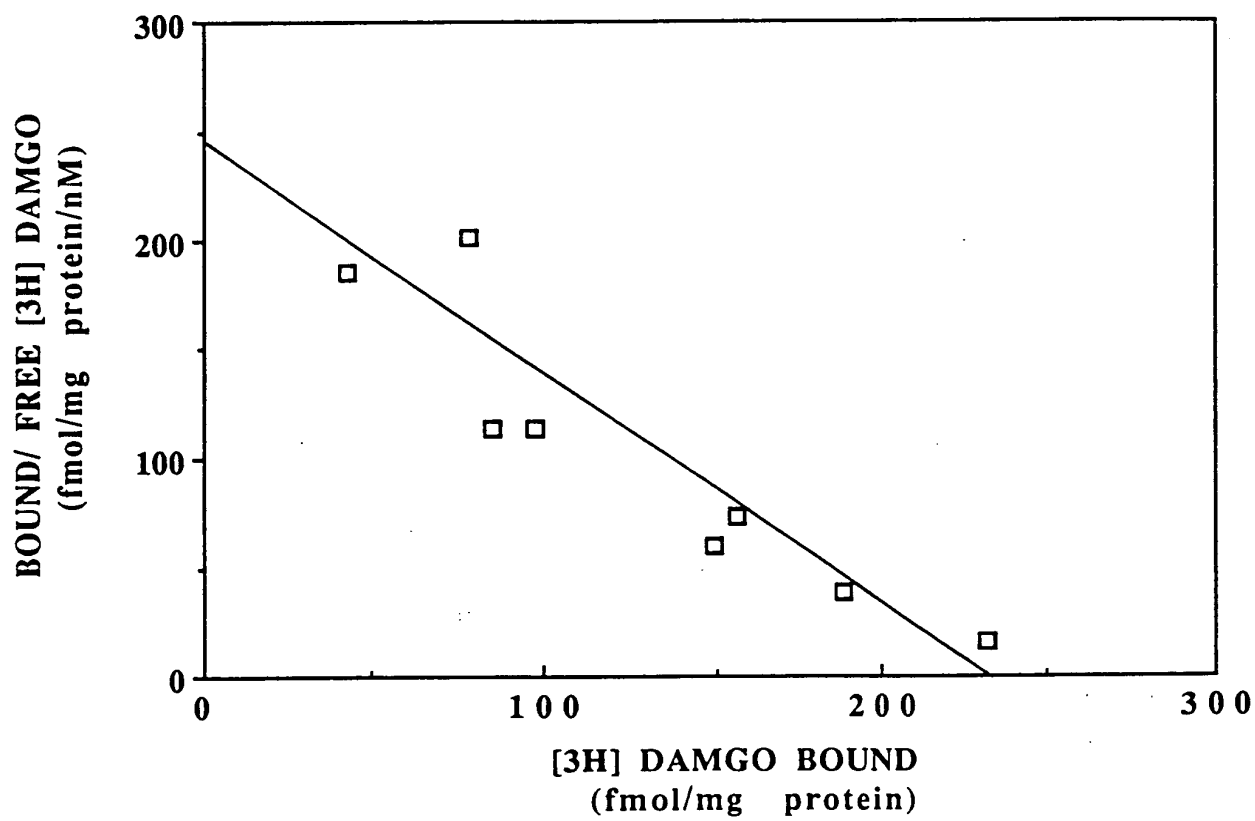
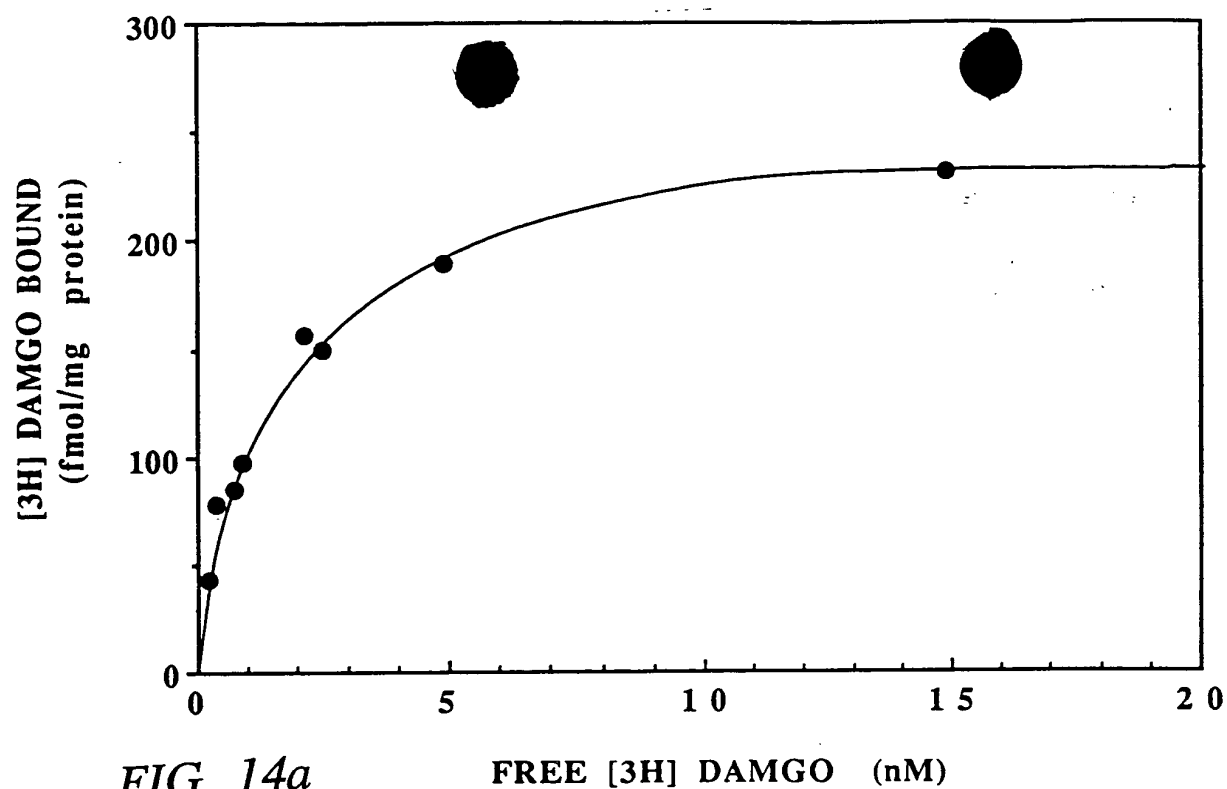


FIG. 13



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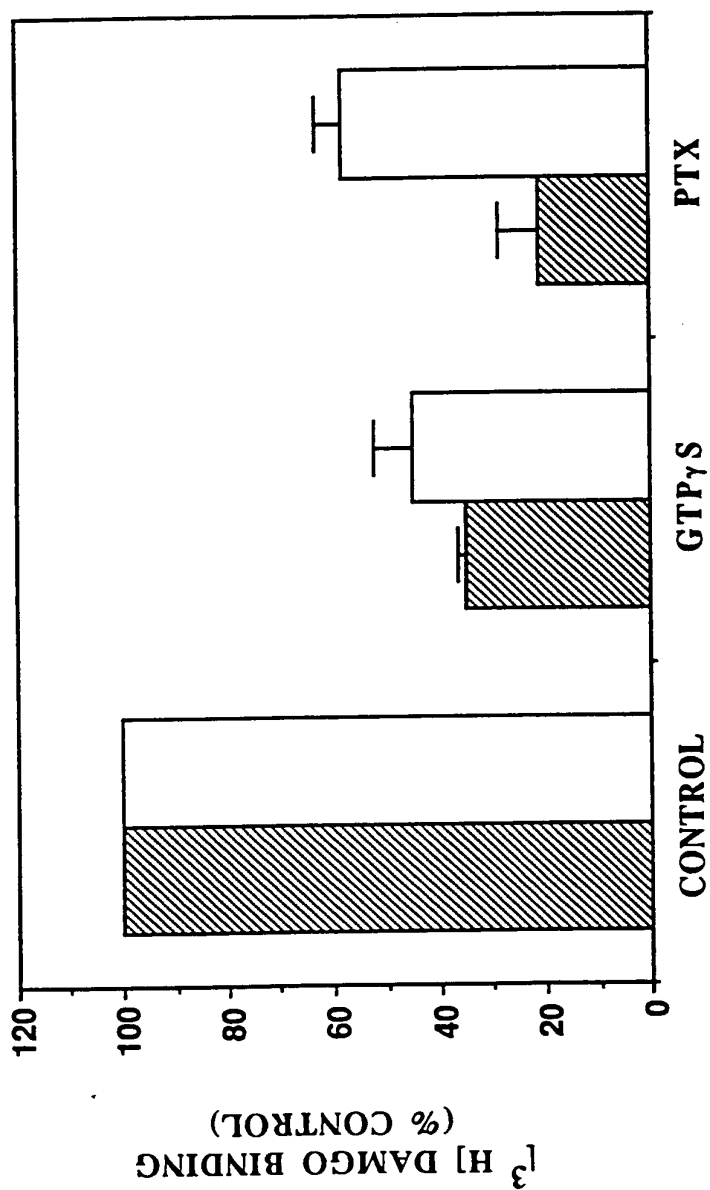


FIG. 15

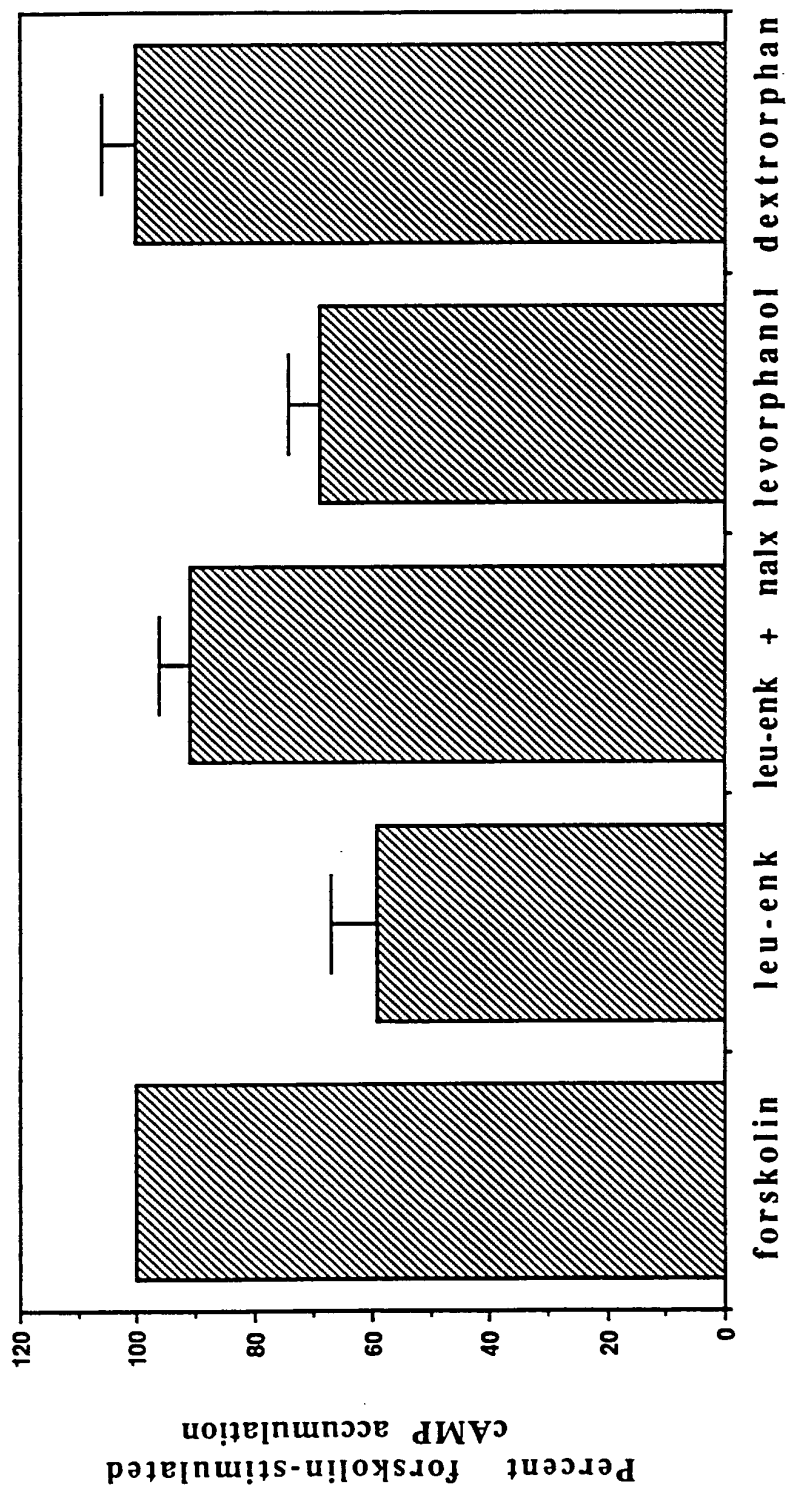


FIG. 16

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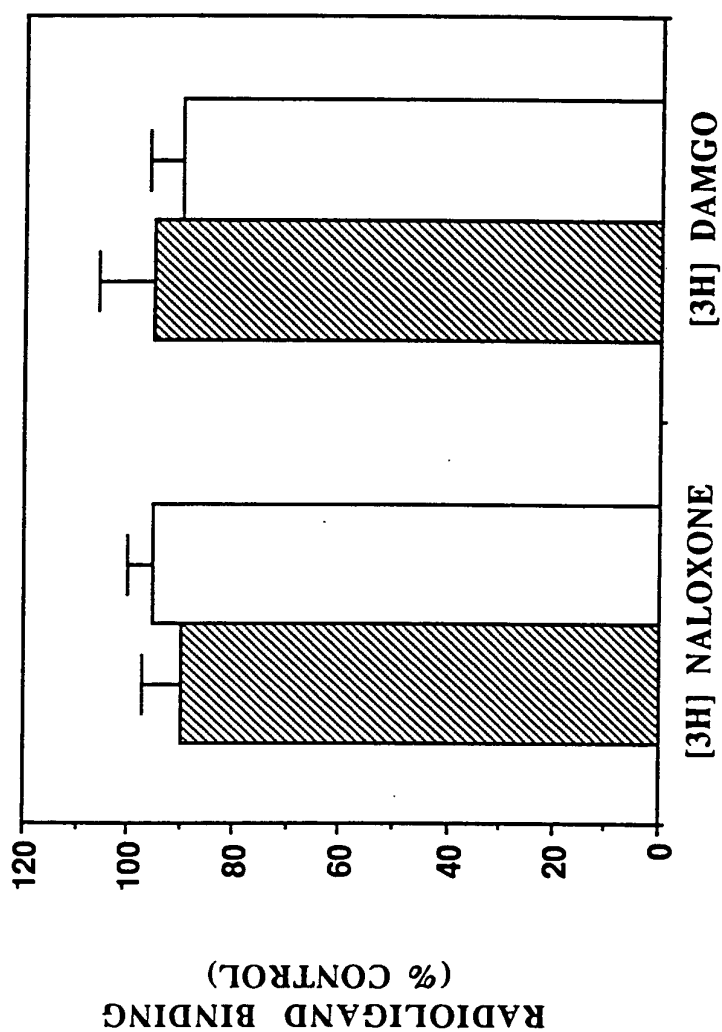


FIG. 17

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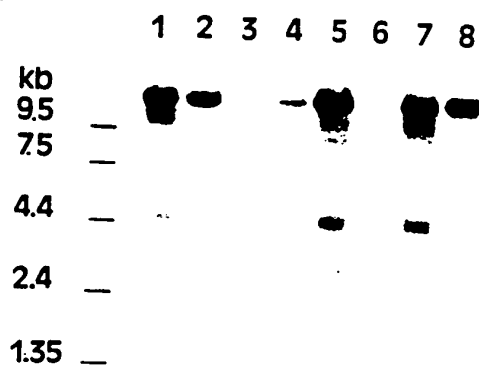


FIG. 18